[

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Sat May 13 08:34:56 2000; MasPar time 21.20 Seconds 659.132 Million cell updates/sec

Title:

Description:
Perfect Score:
Sequence:

>US-09-331-631-8 (1-590) from US09331631.pep (1 of 4) 4332 1 MVRNKSACVVLLFSLFLSFG.....FNSNPQESYFVSRQRQRASE 590

Scoring table: PAM 150 Gap 11

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

188963 segs, 23686106 residues

Database: a-geneseq35 1:geneseqp

Statistics: Mean 36.568; Variance 172.610; scale 0.212

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

PA (RETER') COOP RES CENT TROPICAL PLANT PATHOLOGY. PI BOWER NI, Goulter KC, Green JL, Manners JM, Marcus JP; PR WPI; 98-377279/32. PT Novel anti-microbial protein from e.g. Macadamia integrifolia - PT useful for controlling microbial infestations of plants or mammal S Claim 1; Page 49-51; 96pp; English. CC The sequence is that of an antimicrobial protein which can CC animals. SQ Sequence 590 AA; Query Match Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 590; Conservative 0; Mismatches 0; Indels 0; Ga Db 1 MVRNKSACVVLLFSLFLSFGJLCSAKDFPGRRGDDDPKRYEDCRRRCEWDTRGQKEQQO Db 1 MVRNKSACVVLLFSLFLSFGJLCSAKDFPGRRGDDDPKRYEDCRRRCEWDTRGQKEQQO Db 1 MVRNKSACVVLLFSLFLSFGJLCSAKDFPGRRGDDDPKRYEDCRRRCEWDTRGQKEQQO Db 1 MVRNKSACVVLLFSLFLSFGLLCSAKDFPGRRGDDDPKRYEDCRRRCEWDTRGQKEQQO Db 1 MVRNKSACVVLLFSLFLSFGLLCSAKDFPGRRGDDDPKRYEDCRRCEKRFEQEQQOS Db 121 QRQFQECQHCHQQEQRREKQQCVRECREKYQENPWRGEREEEABEEETEEGEQEQSHN Db 121 QRQFQECQHCHQQEQRPEKKQQCVRECREKYQENPWRGEREEEABEEETEEGEQEQSHN Db 121 QRQFQECQHCHQQEQRPEKKQQCVRECREKYQENPWRGEREEEABEEETEEGEQEQSHN Db 181 PFHFHRRSFQSRFREEHGNFRVLQRFASRHPILRGINEFRLSILEANPNTFVLPHHCDAE Db 181 PFHFHRRSFQSRFREEHGNFRVLQRFASRHPILRGINEFRLSILEANPNTFVLPHHCDAE Db 241 KIYLVTNGRGTLTFLTHENKESYNIVPGVVKVPAGSTVYLANQDNKEKLLIAVLHRPVN
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(RETR-) COOP RES CEN Bower NI, Goulter KC WPI; 98-377279/32. Novel anti-microbial useful for controlli Claim 1; Page 49-51; The sequence is that be used to control m animals. Sequence 590 AA;
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(RETR-) COOP RES CEN Bower NI, Goulter KC WPI; 98-377279/32. Novel anti-microbial useful for controlli- Claim 1; Page 49-51;
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Claim 4; Fig 2; 59pp; English.

The inventors claim a 67 kD and 31 kD T. cacao protein, and fragments, and encoding DNAs. The 47 kD and 31 kD proteins are derived from the 67 kD precursor. T. cacao protein cDNA was derived in a cDNA library prepared from immature cocoa beans RNA using a probe based on the AA sequence of a CNBr peptide common to the 47 kD and 31 kD polypeptides. Homology searches revealed close homologies between the 67 kD polypeptide and the vicilins, which are
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11-JUN-1990; GB-013016.
(MRSC ) MARS UK LTD.
Spencer ME, Hodge R, Deakin
WPI; 92-024418/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
261; Conser
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22-DEC-1997; AU0874
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPIC
Bower NI, Goulter KC, Green
WPI; 98-377279/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Theobroma cacao antimicrobial protein antimicrobial protein; infestation; co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be used to control microbial infestations animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel anti-microbial protein from e.g. Macadamia integruseful for controlling microbial infestations of plants Claim 1; Page 47-49; 96pp; English.

The sequence is that of an antimicrobial protein which
KAPLSPGDVFVAPAGHAVTFFASKDQPLNAVAFGLNAQN
                                                                                                                                                                                                                                                                                                              VPHYNSKATFVVFVTDGYGYAQMACPHLSRQSQGSQSGRQDRREQEEESEEETFGEFQQV
                                                                                                                                              EATSPREKSGERFAFULLSQTPRYSNQNGRFFEACPPEFRQLRDINVTVSALQLNQGSIF
                                                                                                                                                                      QATSPRHRGGERLAINLLSQSPVYSNQNGRFFEACPEDFSQFQNMDVAVSAFKLNQGAIF
                                                                                                                                                                                                                                                       FRDEEGNFKILQRFAENSPPLKGINDYRLAMFEANPNTFILPHHCDAEAIYFVTNGKGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPRQQYEQCQRRCESEATEEREQEQCEQRCEREYKEQQRQQEEELQRQYQQCQGRCQEQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QATSPRHRGGERLAINLLSQSPVYSNQNGRFFEACPEDFSQFQNMDVAVSAFKLNQGAIF
                                                             VPHYNSKATFVILVTEGNGYAEMVSPHLPRQSSYEEEEEEDEEEEQEQEEERRSGQYRKI
                                                                                                                                                                                                                               SQRPQSYLRAFSREILEPAFNTRSEQLDELFGGRQSRRRQQGQ-GMFRKASQEQIRALSQ
                                                                                                                                                                                                                                                                                                                                                                                                    FREEHGNFRVLQRFASRHPILRGINEFRLSILEANPNTFVLPHHCDAEKIYLVTNGRGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QRPEKKQQCVRECREKYQENPWRGEREE-EAEEEE-TEEGEQEQSHNPFHFH-RRSFQSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGQREQQQCQRKCWEQYKEQE-RGEHENYHNHKKNRSEEEEGQQRNNPYYFPKRRSFQTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPQRRYEECQQEC-RQQ-EERQQPQCQQRCLKRF-EQE-QQQS--QRQFQECQQHCHQQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPHYNSKATFVILVTEGNGYAEMVSPHLPRQSSYEEEEEEDEEEEQEQEEERRSGQYRKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EATSPREKSGERFAFNLLSQTPRYSNQNGRFFEACPPEFRQLRDINVTVSALQLNQGSIF
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llarity 56.98;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1910; DB 1;
Pred. No. 4.54e-157;
95; Mismatches 92:
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                     494
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plants or mar
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Best Local S
Matches 22
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AETR-) COOP RES CENT TRO.

BOWER NI, GOULTER KC, Gree.

WPI; 98-377279/32.

N-PSDB; V42310.

Novel anti-mi-

Lai-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel anti-microbial protein from e.g. Macadamia int useful for controlling microbial infestations of pla Claim 1, Page 34-36, 96pp; English.

The sequence is that of an antimicrobial protein whi be used to control microbial infestations in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macadamia integrifolia antimicrobial protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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              624
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 VEESFNSQDQSIFFPGPRQHQQQS
                                                                                                                                                                             PAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALN
                                                                                                                                                                                                                                                                                                                                             GRGGDMMNPQRGGSGRYEEGEEEQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLL
                                                                                                                                                                                                                                                                                                                                                                                  PVVFVSSGNENLLLFAFGINAQN-N--H-EN-FLAGRERNVLQQIEPQAMELAFAAPRKE
                                                                                                GEADVEMACPHL---SG--RHGGRGGGKRHEEEED--V-HYEQVRARLSKREAIVVLAGH
                                                                                                                              LLSQTPRYSNQNGRFFEACPPEFRQLRDINVTVSALQLNQGSIFVPHYNSKATFVILVTE
                                                                                                                                                                                                                                                                                      RALKNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRI
                                                                                                                                                                                                                                                                                                                                                                                                                    DPPKRYEDCRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHRPEDPQRRYEECQQECR 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSRLSRGDIFVVPANFPVTFVASQNQNLRMTGFGLYNQN 530
                                                                                 GNGYAEMVSPHLPRQSSYEEEEEEDEEEEEQEQEEERRSGQYRKIRSRLSRGDIFVVPANF
                                                                                                                                                      LFNKRPLYSNKYGQAYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVAS
                                                                                                                                                                                                                           PAGSTVYLANQDNKEKLIIAVLHRPVNNPGQFEEFFPAGSQRPQSYLRAFSREILEPAFN
                                                                                                                                                                                                                                                                           RGINEFRLSILEANPNTFVLPHHCDAEKIYLVTNGRGTLTFLTHENKESYNIVPGVVVKV
                                                                                                                                                                                                                                                                                                                        PWRGER-EEEAEEEET-EEGEQEQSHNPFHFHRRSFQSRFREEHGNFRVLQRFASRHPIL
                                                                                                                                                                                                                                                                                                                                                                     QQEERQQPQCQQRCLKRFEQEQQQSQRQFQECQQHCHQQEQRPEKKQQCVRECREKYQEN
                                   PVTFVASQNQNLRMTGFGLYNQNINPDHNQRIFVAGKINHV-RQWDSQAKELAFGVSSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; infestation;
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29. .666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1246; DB 1;
Pred. No. 3.18e-97;
150; Mismatches 144
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, Manners JM, Marcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 144;
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Best Local :
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The sequence is that of an antimicrobial p be used to control microbial infestations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          animals.
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22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT T
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27-OCT-1998
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VEELFNSQDESIFFPGPRQHQQQS
                                                                                                                                                                                                                                                                                                                                                                                                                                PVVFVSSGNENLLLFAFGINAQN-N--H-EN-FLAGRERNVLQQIEPQAMELAFAASRKE
                                                                                GNGYAEMVSPHLPRQSSYEEEEEEDEEEEQEQEEERRSGQYRKIRSRLSRGDIFVVPANF
                                                                                                       GEADVEMACPHL ---
                                                                                                                             LISQIPRYSNQNGRFFEACPPEFRQIRDINVIVSALQLNQGSIFVPHYNSKATFVILVIE
                                                                                                                                            LFNKRPLYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVAS
                                                                                                                                                                           TRSEQLDELFGGRQSRRRQQGQGMFRKASQEQIRALSQEAT-SPR-E--KSGE--RFAFN
                                                                                                                                                                                                 TQTERLRGVLG--Q--QRE-G-VIIR-ASQEQIRELTRDDSESRRWHIRRGGESSRGPYN 415
                                                                                                                                                                                                                                          PAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALN
                                                                                                                                                                                                                                                                                     RALKNYRLVLLEANPNAFYLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRI
                                                                                                                                                                                                                                                                                                                      PWRGE-REEEAEEEET-EEGEQEQSHNPFHFHRRSFQSRFREEHGNFRVLQRFASRHPIL
                                                                                                                                                                                                                                                                                                                                  GRGGDLMNPQRGGSGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLL 242
                                                                                                                                                                                                                                                                                                                                                                    QQEERQQPQCQQRCLKRFEQEQQQSQRQFQECQQHCHQQEQRPEKKQQCVRECREKYQEN
                                                                                                                                                                                                                                                                                                                                                                                    EDEEK----YEER-MKEGDNKRDPQQREYEDCRRHCEQQEPRLQ--YQCQRRCQEQQRQH 182
                                                                                                                                                                                                                                                                                                                                                                                                                  DPPKRYEDCRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHRPEDPQRRYEECQQECR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDEIFNSNPQESYFVS-RQRQRAS
                                                                                                                                                                                                                          PAGSTVYLANQDNKEKLIIAVLHRPVNNPGQFEEFFPAGSQRPQSYLRAFSREILEPAFN
                                                                                                                                                                                                                                                                          RGINEFRLSILEANPNTFVLPHHCDAEKIYLVTNGRGTLTFLTHENKESYNIVPGVVVKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 28.7%; similarity 39.9%; 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     integrifolia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                       -SG--RHGGRGGGKRHEEEEE--V-HYEQVRARLSKREAIVVLAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Green JL,
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اا
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infestation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1244; DB 1; I
Pred. No. 4.80e-97;
149; Mismatches 143;
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Best Local Similarity 39.4%;
Matches 222; Conservative
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W62829 stand
W62829;
27-OCT-1998
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The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammal
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WPI; 98-377279/32.
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20-DEC-1996; AU-004275.
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                                                                           PVTFVASQNQNLRMTGFGLYNQNINPDHNQRIFVAGKINHV-RQWDSQAKELAFGVSSRL
                                                                                                    PVVFVSSGNENLLLFAFGINAQN-N--H-EN-FLAGRERNVLQQIEPQAMELAFAAPRKE
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D 02-JUL-1997; AUU874.

F 22-DEC-1997; AU-004275.

R 20-DEC-1996; AU-004275.

A (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.

A (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.

Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;

Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;

R WPI, 98-377279/32.

T Novel anti-microbial protein integrifolia microbial infestations of plants or man useful for controlling microbial protein which can S Claim 1; Page 63-65; 96pp; English.

C The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammal
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168; Mismatches 164
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Zea mays.

Wo9877805-Al.

WO9877805-Al.

22-JUL-1998.

22-DEC-1997; AUU874.

20-DEC-1996; AU-004275.

(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.

(RETR-) COUNTER KC, Green JL, Manners JM, Maj
                                                                                   29-DEC-1997 (first entry)
Peanut allergen Ara hI.
Peanut seed storage protein; allergen; allergy; hypersensitivity;
vaccine; anaphylactic shock; immunotherapy; therapy;
monoclonal antibody; ELISA; analysis; Ara hI.
Arachis hypogaea strain Florunger.
                                                                                                                                                                                                                                                                       W22149 standard; Protein; 614 W22149;
  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for controlling microbial infestations of plants Claim 1; Page 58-60; 96pp; English.
The sequence is that of an antimicrobial protein which be used to control microbial infestations in plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-OCT-1998 (first entry)
Zea mays antimicrobial protein.
antimicrobial protein; infestation; control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bower NI, Goulter KC, Green WPI; 98-377279/32.
                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                 576
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  /label= Sig_peptide
23. .614
                                                                             Location/Qualifiers
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Pred. No. 3.17e-71;
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Claim 31; Page 169; 354pp; English.
Claim 31; Page 169; 364pp; English.
Claim 40; 364pp; English.
Claim 51; Page 169; 364pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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10-JUL-1997.
23-SEP-1996; U15222.
04-MAR-1996; US-610424.
29-DEC-1995; US-009455.
(UVAR-) UNIV ARKANSAS.
Bannon GA, Burks AW, CWPI; 97-363453/33.
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                                                                                                                     EKLIK-NQRESHFVSARPQSQS 586
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                                                                                                                                                                                 VTFVASQNQNLRMTGFGLYNQNINPDHNQRIFVAGKINHVR-QWDSQAKELAFGVSSRLV
                                                                                                                                                                                                                                                                         NGYAEMVSPHLPRQSSYEEEEEEEDEEEEQEQEEERRSGQYRKIRSRLSRGDIFVVPANFP
                                                                                                                                                                                                                                                                                                                                                                  SQTPRYSNONGRFFEACPPE-FROLRDINVTVSALQLNQGSIFVPHYNSKATFVILVTEG
                                                                                                                                                                                                                                                                                                                                                                                              DGEPDLSNNFGRLFEVKPDKKNPQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVVNKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NQNLRVAKISMPVNTPGQFEDFFPASSRDQSSYLQGFSRNTLEAAFNAEFNEIRRVLLEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEQEQQQSQRQFQECQQHCHQQE-QRPEKKQQCVRECREKYQENPWRGEREE-EAEEE-E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 834; DB 1;
Pred. No. 1.73e-60;
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Peptide;

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Best Local S
Matches 17
                                       Peanut allergen Ara hI.
Peanut; seed storage protein; allergen; allergy; hypersensitivity;
vaccine; anaphylactic shock; immunotherapy; therapy;
monoclonal antibody; ELISA; analysis; Ara hI.
Arachis hypogaea strain Florunger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
BOWER NI, Goulter KC, Green JL, Manners JM, Marcus JP;
WPI; 98-377279/32.
Novel anti-microbial protein from e.g. Macadamia integrifolia -
                                                                                                               W22150;
29-DEC-1997
                                                                                                                                             W22150 standard; Protein; 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for controlling microbial infestations of plants or mammal Claim 1; Page 55-57; 96pp; English.
The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antimicrobial pro
Arachis hypogaea.
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Arachis hypogaea antimicrobial protein.
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27-OCT-1998
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02-JUL-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity les 178; Conser
                                                                                                                                                                                                                        EKLIK-NQRESHFVSARPQSQS
                                                                                                                                                                                                                                                            DGEPDLSNNFGRLFEVKPDKKNPQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVVNKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPNTLVLPKHADADNILVIQQGQATVTVANGNNRKSFNLDEGHALRIPSGFISYILNRHD 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPGSEVREETSRNNPFYFPSRRFSTRYGNQNGRIRVLQRFDQRSKQFQNLQNHRIVQIEA 213
                                                                                                                                                                                                                                                                                                                      NGYAEMVSPHLPRQSSYEEEEEEDEEEEQEQEEERRSGQYRKIRSRLSRGDIFVVPANFP
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                                                                                                               (first entry)
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1. .22
/label=
                           Location/Qualifiers
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Sig_peptide
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No. 1.73e-60;
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RESULT
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W90342 standard; W90342; 24-MAY-1999 (first e G. max truncated SBP2

protein; entry)

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Best Local :
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This polypeptide comprises major peanut allergen
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(UYAR-) UNIV ARKANSAS.
Bannon GA, Burks AW,
WPI; 97-363453/33.
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23-SEP-1996;
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 SNPQESYFVSRQRQRASE
                                                                                                                                  WYSPHLPRQSSYEEEEEEDEEEEQEQEEERRSGQYRKIRSRLSRGDIFVVPANFPVTFVA
                                                                                                                                                                                                                    LSNNFGKLFEVKPDKKNPQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVVNKGTGNLE
                             -NOKESHFVSARPQSQSQ 592
                                                                 SQNQNLRMTGFGLYNQNINPDHNQRIFVAGKINHVR-QWDSQAKELAFGVSSRLVDEIFN
                                                                                  S-SE-LHLLGFG-----INAENNHRIFLAGDKDNVIDQIEKQAKDLAFPGSGEQVEKLIK
                                                                                                                                                                LVAVRKEQQQR-GRREEEEDEDEEE-EGSNR--EVRRYTARLKEGDVFIMPAAHPVAINA
                                                                                                                                                                                                                                                                                                  ERGQRRWSTRSSENNEGVIVKVSKEHVEELTKHAKSVSKKGSEEEGDITNPINLREGEPD
                                                                                                                                                                                                                                                                                                                                   VLHRPVNNPGQFEEFFPAGSQRPQSYLRAFSREILEPAFNTR-SE--Q--LDELFGG---
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1 Similarity 36.3%;
159; Conservative
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US-610424.
US-009455.
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521. .523
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Pred. No. 4.56e-56;
117; Mismatches 129
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RESULT
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                                                                           SBP1; sucrose binding protein; SBP2; seed; carbohydrate content; soybean. Glycine max:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested, such as syybean). In contrast, decreased sucrose uptake activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAY-1997; US-047568.
(UNIW ) UNIV WASHINGTON STATE RES FOUND.
Chao WS, Grimes HD;
WPI; 99-070155/06.
26-NOV-1998.
21-MAY-1998; U10465.
22-MAY-1997; US-047568
                                                         WO9853086-A1.
                                                                                                                                                                        W90341 standard; W90341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         harvested. The SBP regulatory regions confer specific or enhanc expression in developing seeds and so may be used to express any transgene in developing seeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant harvested. The SBP regulatory regions confer specific or enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a novel sucrose binding protein, SBP2 isol from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New modified plant sucrose binding proteins - used to transgenic plants which can have enhanced or decreased uptake activity in developing seeds Claim 7; Page 39-40; 58pp; English.
                                                                                                                                                      24-MAY-1999
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21-MAY-1998; U10465
22-MAY-1997; US-047
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                                                                                                                                                                                                                                                                                                                                                 347
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                                                                                                                                  max SBP2 protein
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                                                                                                                                                                                                                                                                                           VGPDDEKSWLQRLNLMLTFTNITQRSMSTIHYNSHATKIALVMDGRGHLQISCPHMSSRS
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                                                                                                                                                                                                                                                                                                                                                                                                                      NEKLLLAMLHIPVSTPGKFEEFFGPGGRDPESVLSAFSWNVLQAALQTPKGKLERLFN-Q 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPNTFVLPHHCDAEKIYLVTNGRGTLTFLTHENKESYNIVPGVVVKVPAGSTVYLANQDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAHTFVSPRHFDSEVVLFNIKGRAVLGLVRESETEKITLEPGDMIHIPAGTPLYIVNRDE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EETEEGEQEQSHNPFHFHR-RSFQSRFREEHGNFRVLQRFASRHPILRGINEFRLSILEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EHQEQHEEEEDENPYVFEEDKDFSTRVETEGGSIRVLKKFTEKSKLLQGIENFRLAILEA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKRFEQEQQQSQRQFQECQQHCHQQEQRPEK-KQQCVRECREKYQENPWRGEREE-EAEE 167
                                                                                                                                                                                                                                                                                                                                               QSRRRQQGQGMFRKASQEQIRALSQEATSPR-EKSGE-RFAFNLLSQTPRYSNQNGRFFE
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128; Conser
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larity 35.6%;
Conservative
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Pred. No. 4.88e-54
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                                                                                                                 sucrose uptake;
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RESULT
ID WE
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KW HE
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PD 0:
PPF 2:
PPR 2:

W62837 standard;

Protein;

637

A

antimicrobial protein; infestation; control

Hordeum vulgare antimicrobial protein

27-OCT-1998 (first entry)

Hordeum vulgare. W09827805-A1.

02-JUL-1998. 22-DEC-1997; AU0874. 20-DEC-1996; AU-004275

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Best Local
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WPI; 99-070155/06
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Claim 13b; Page 37-38; 58pp; English.
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524 FGLYNQNINPDHNQRIFVAGKINHVRQWDSQAKELAFGVSSRLVDEIFNSNPQESYF
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                                              IC-FEVNVR-DNKKFTF-AGKDNIVSSLDNVAKELAFNYPSEMVNGVSERK-ESLFF 474
                                                                                                                                                                                                                                       VGPDDEKSWLQRLNLMLTFTNITQRSMSTIHYNSHATKIALVMDGRGHLQISCPHMSSRS
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                                                                                               SYEEEEEEDEEEEQEQEEERRSGQYRKIRSRLSRGDIFVVPANFPVTFVASQNQNLRMTG
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161; Conser
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33.8%;
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Pred. No. 2.65e-54;
129; Mismatches 154
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Best Local :
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                                                                      o. max SBP1 protein.
SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean.
Glycine max.
                                                                                                                                                  W90339;
26-NOV-1998.
21-MAY-1998; U10465.
22-MAY-1997; US-047568.
(UNIW ) UNIV WASHINGTON
                                                            WO9853086-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel anti-microbial protein from e.g. Macadamia integrifolia useful for controlling microbial infestations of plants or man Claim 1; Page 60-62; 96pp. English.

The sequence is that of an antimicrobial protein which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY. Bower NI, Goulter KC, Green JL, Manners JM, Mar WPI; 98-377279/32.
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                                                                                                                                                                                                                                                                                                      PVVEISS-SQG-S-SNLQVVCFEINAERNERVWLAGRNNVIGKLGSPAQELTFGRPAREV
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                                                                                                                                                                                                                                                                                   PVTFVASQNQNLRMTGFGLYNQNINPDHNQRIFVAGKINHVRQWDSQAKELAFGVSSRLV
                                                                                                                                                                                                                                                                                                                                          SSYEEEEEED---EEEEQEQEEERRSG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGQGMFRKASQEQIRALSQEAT--SP--R-E-KS--GE-RFAFNLLSQTPRYSNQNGRFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HHCDAEKI-YLVTNGRGTLTFLTHENKESYNIVPGVVVKVPAGSTVYLANQDNKEKLIIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNKSACVVLLFSLFLSFGLLCSAKDFPGRRGDDDPPK-R-YEDCRRRCEWDTRGQKEQQQ
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                                                                                                                                                                standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 17.5%;
l Similarity 31.6%;
197; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 637 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           control microbial infestations in plants and mammalian
   STATE RES FOUND
                                                                                                                                                                 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 758; DB 1; Lo
Pred. No. 8.97e-54;
l65; Mismatches 205;
                                                                                                                                                                                                                           590
                                                                                                                                                                 AA
                                                                                                                                                                                                                                                                                                                                          -----Q-YRKIRSRLSRGDIFVVPANF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.0%;
Best Local Similarity 34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a novel sucrose binding protein, SBP1 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uptake activity in developing seeds Disclosure; Page 34-36; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucros
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                                                                                                                                                                                                                                                                                                                                                                                                              MVNGVF 481
                                                                                                                                                                                                                                                                                                                                                     AALQTPKGKLENVFD-QQN----EG-SIFR-ISREQVRALAPTKKSSWWPFGGESKPQFN 313
                                                                                                     GHPFVTIASNKENLLMICFEV---N-ARDNKKFTF-AGKDNIVSSLDNVAKELAFNYPSE 475
                                                                                                                                                                                                                                                                  IFSKRPTISNGYGRLTEVGPDDDEKSWLQRLNLMLTFTNITQRSMSTIHYNSHATKIALV 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRQQE-ERQQPQCQQRCLKRFEQEQQQSQRQFQECQQHCHQ-QEQRPEKKQQCVRECREK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CKETEVEEEDPE-LYTCKHQCQQQQQYTEGDKRVCLQSCDRYHRMKQEREKQIQEETREK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WS, Grimes H
99-070155/06
                                                           NFPVTFVASQNQNLRMTGFGLYNQNINPDHNQRIFVAGKINHVRQWDSQAKELAFGVSSR 565
                                                                                                                                                 TEGNGYAEMVSPHLPRQSSYEEEEEEDEEEEQEQEEERRSGQYRKIRSRLSRGDIFVVPA
                                                                                                                                                                                        IDGRGHLQISCPHMSSRSSH-----S----K-HD--KSSPSYHRISSDLKPGMVFVVPP 420
                                                                                                                                                                                                                                    LLSQTPRYSNQNGREFEACPPEF-RQ-LRDINVTVSALQLNQGSIFVPHYNSKATFVILV
                                                                                                                                                                                                                                                                                                                           PAFNTRSEQLDELFGGRQSRRRQQGQGMFRKASQEQIRALSQEATSPR-EKSGE-RFAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILRGINEFRLSILEANPNTFVLPHHCDAEKIYLVTNGRGTLTFLTHENKESYNIVPGVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YQENPWRGEREEEAEEEETEEGEQEQSHNPFHFHRRSFQSRFREEHGNFRVLQRFASRHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEEES-R-EREEE-QQEQ-HE-EQDENPYIFE-EDKDFETRVETEGGRIRVLKKFTEKSK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  524 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 737; DB 1;
Pred. No. 6.35e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 524;
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Search completed: Sat May 13 08:35:22 Job time: 26 secs.

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